

Fig 1: Ribbon representation of aspartic proteinases in a) Front view and b) Top view.

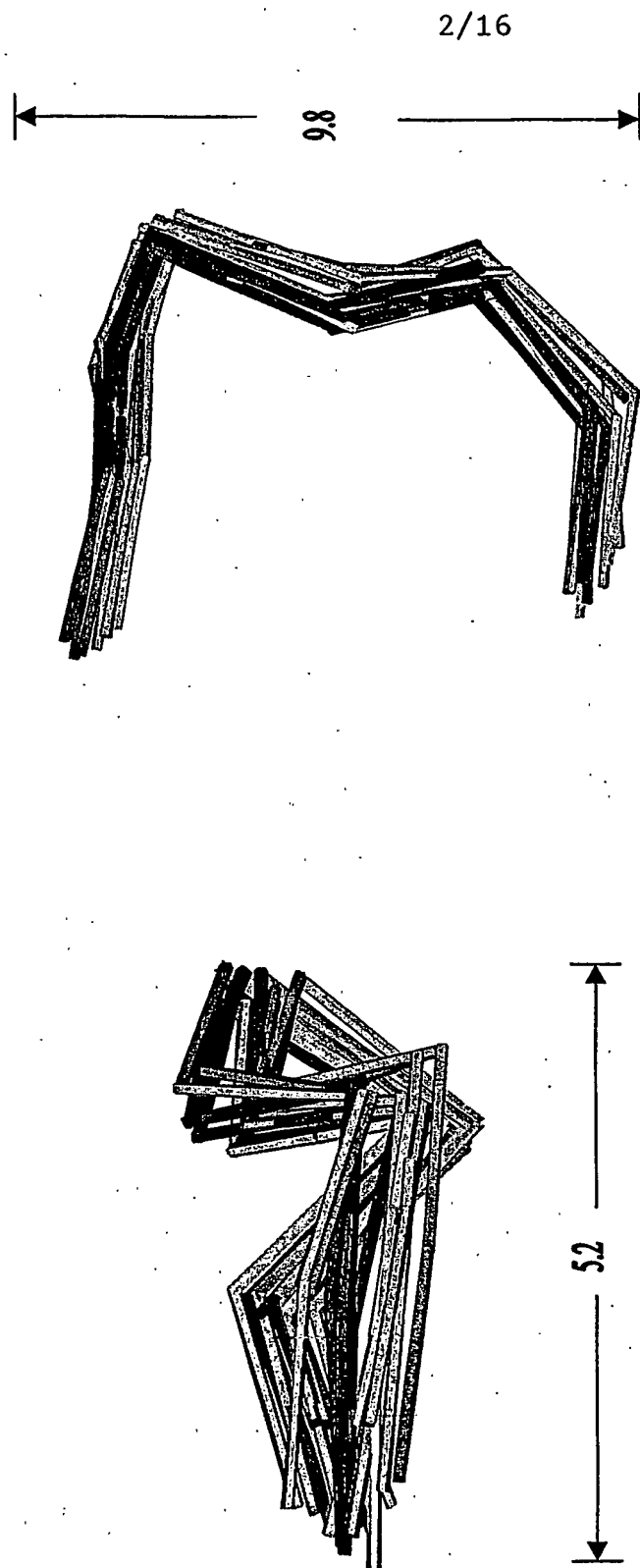


Fig 2a: Residues (217-224) considered as CDPL (C-Domain Plane) in different orientations. Dimensions are expressed in Angstrom units.

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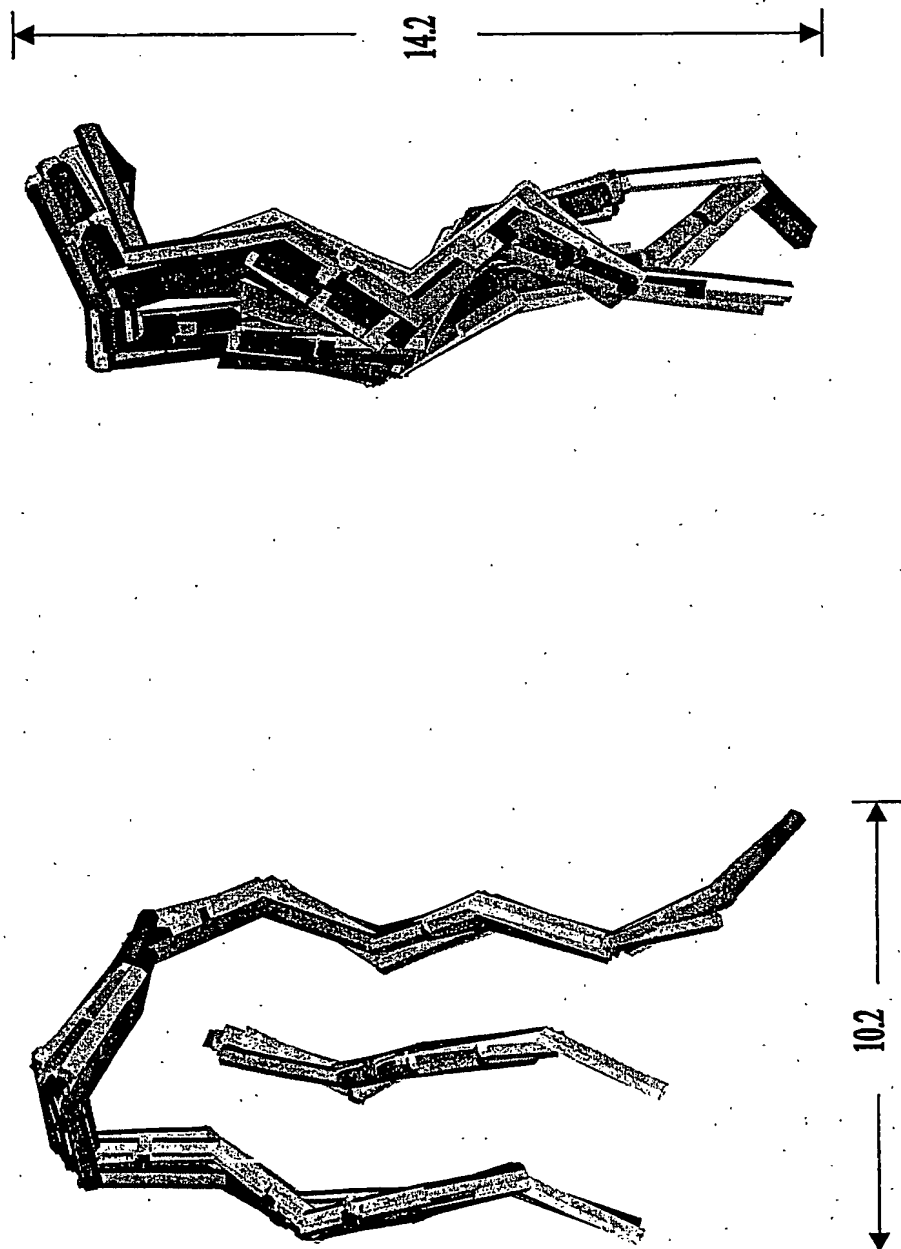


Fig 2b: Residues (32-44, 121-124) considered as NDPL (N-Domain Plane) in different orientations. Dimensions are expressed in Angstrom units.

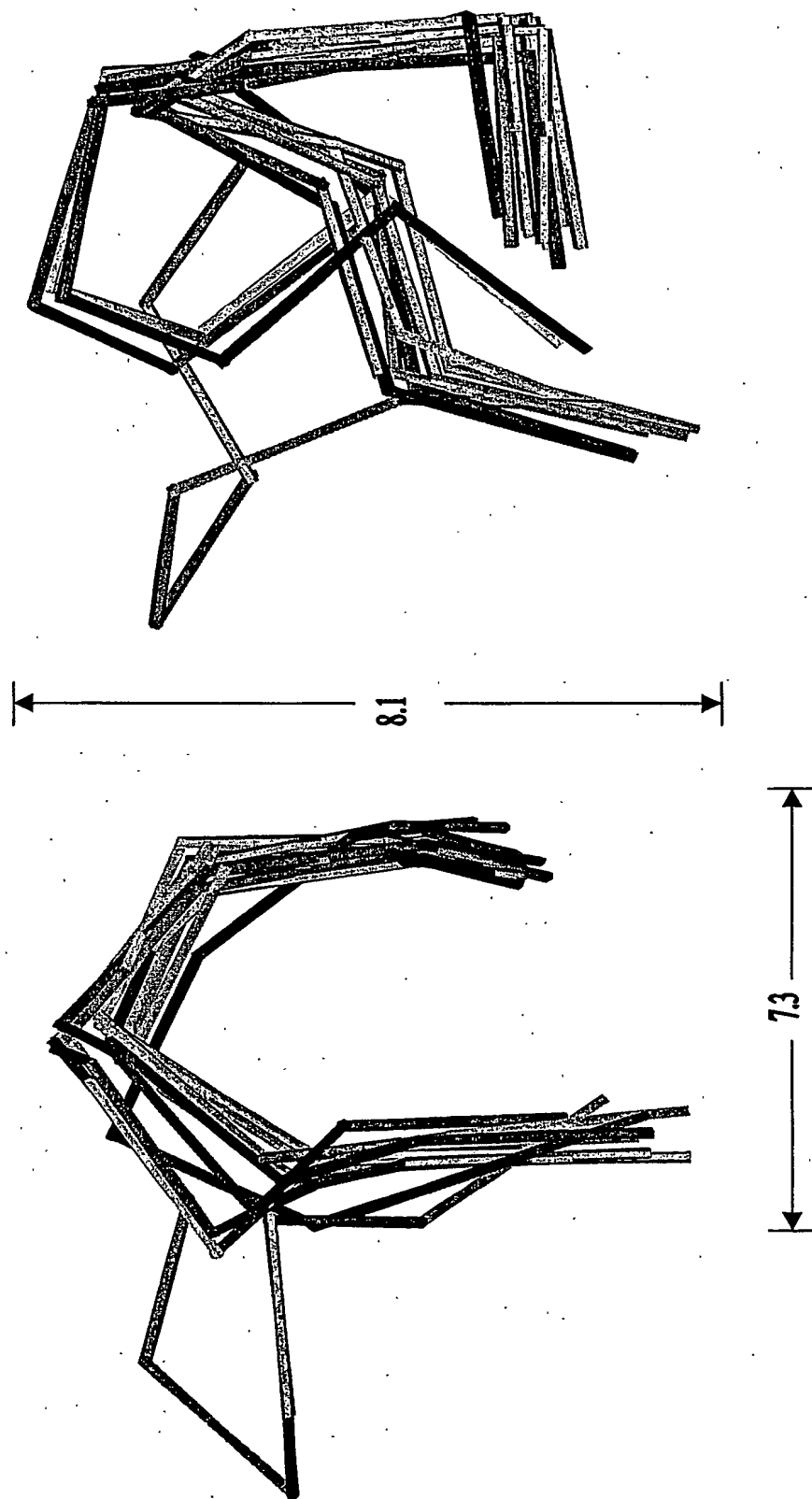


Fig 2c: Residues (189-196) considered as EXPL (Exit Plane) in different orientations. Dimensions are expressed in Angstrom units.

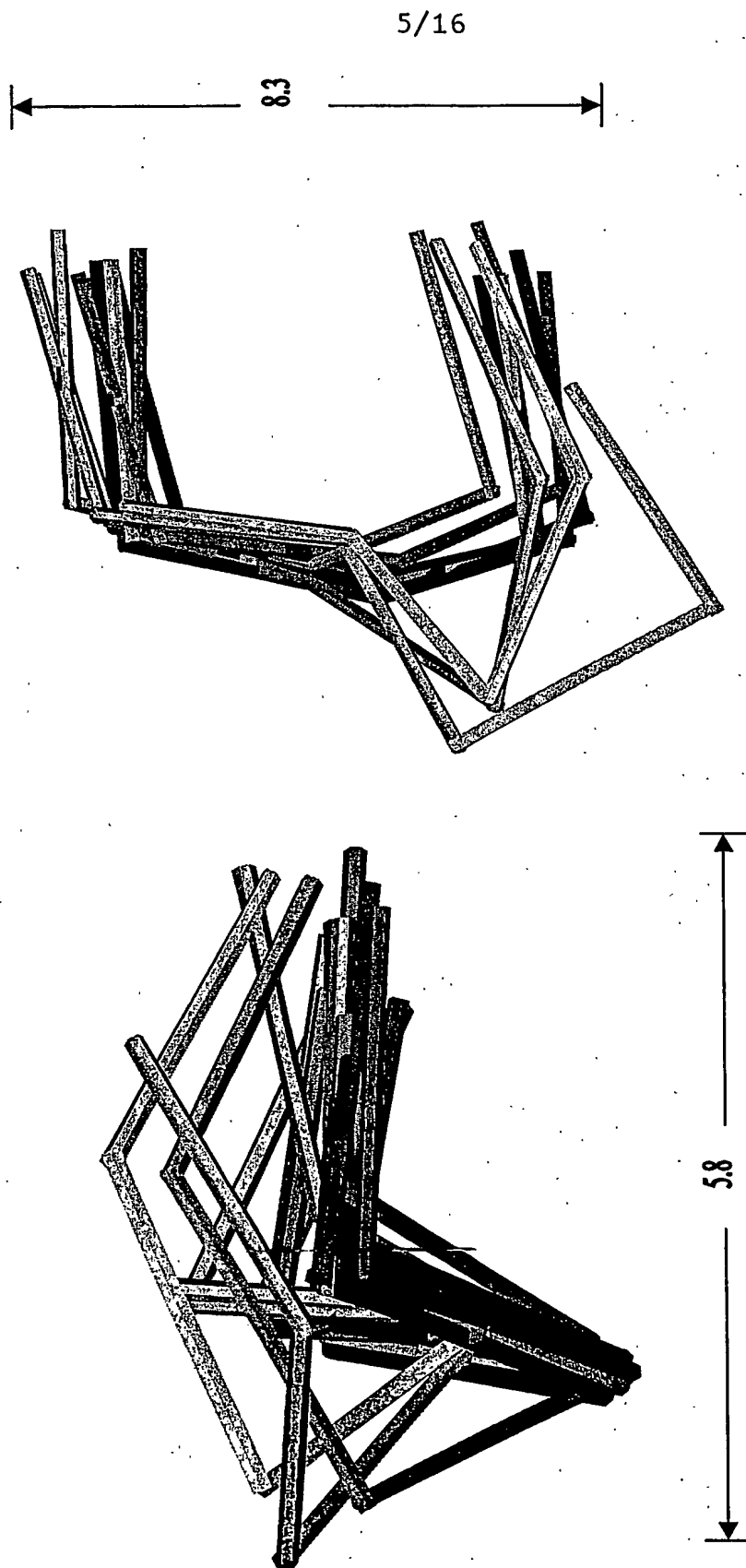


Fig 2d: Residues (11-16) considered as ENPL (Entry Plane) in different orientations. Dimensions are expressed in Angstrom units.

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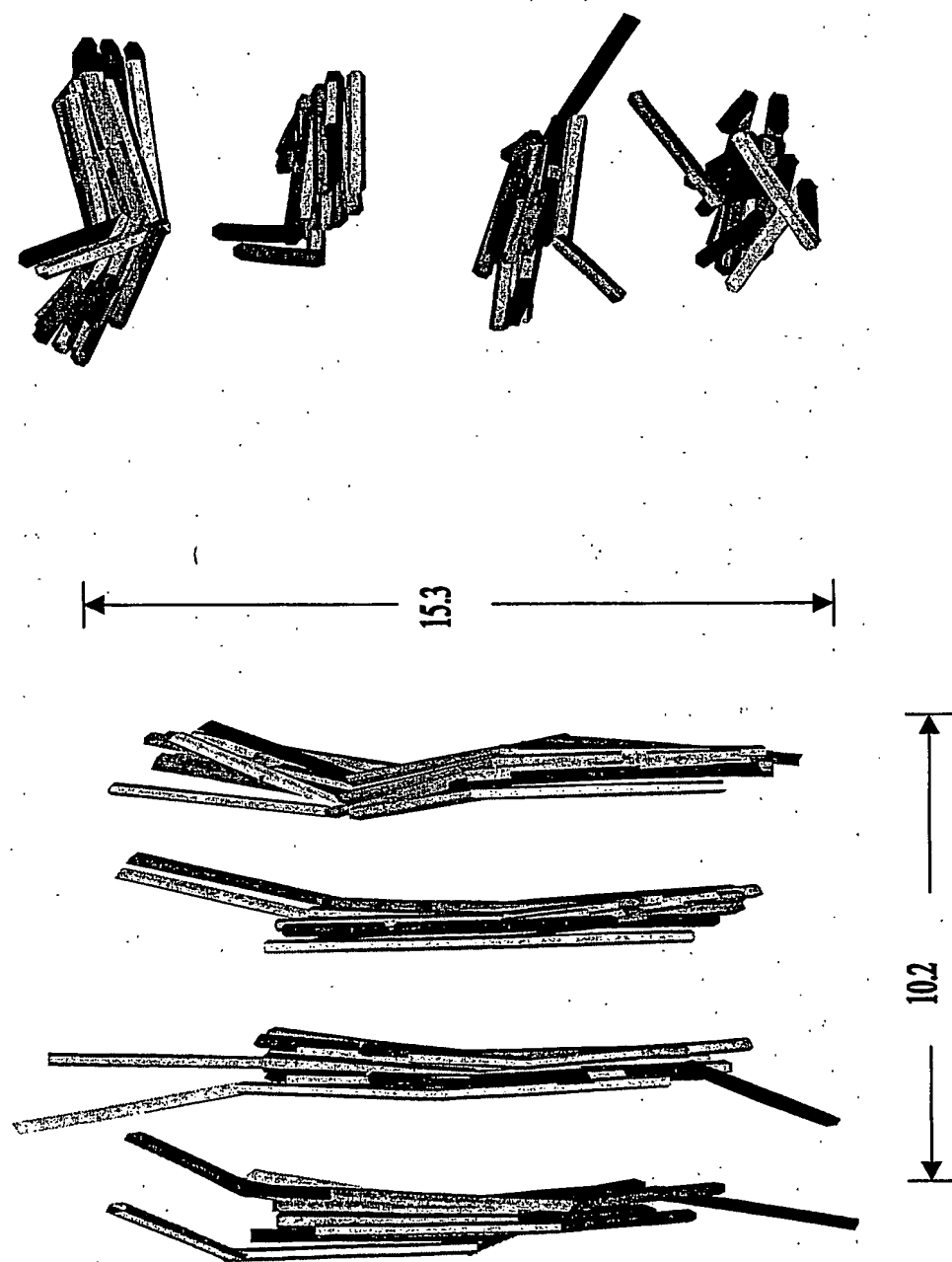


Fig 2e: Residues (214-217, 224-227, 289-292, 297-299) considered as CDWL (C-Domain Wall) in different orientations. Dimensions are expressed in Angstrom units.

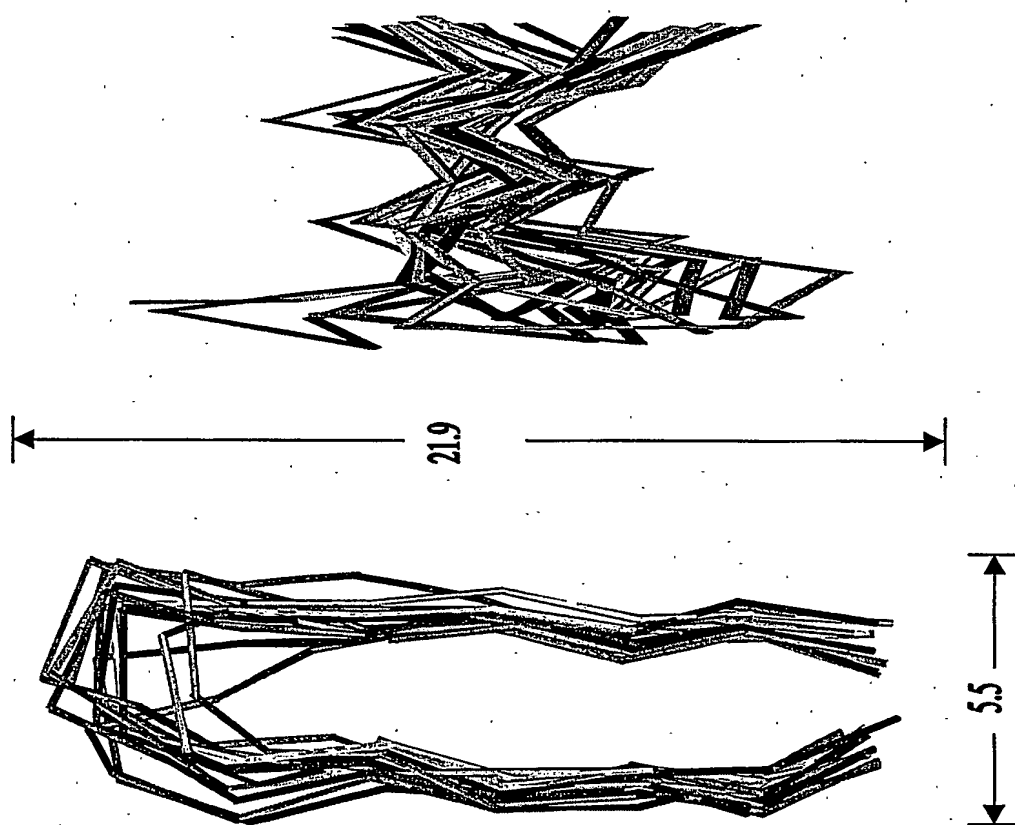


Fig 2f: Residues (72-86) considered as FLAP (Flap) in different orientations. Dimensions are expressed in Angstrom units.

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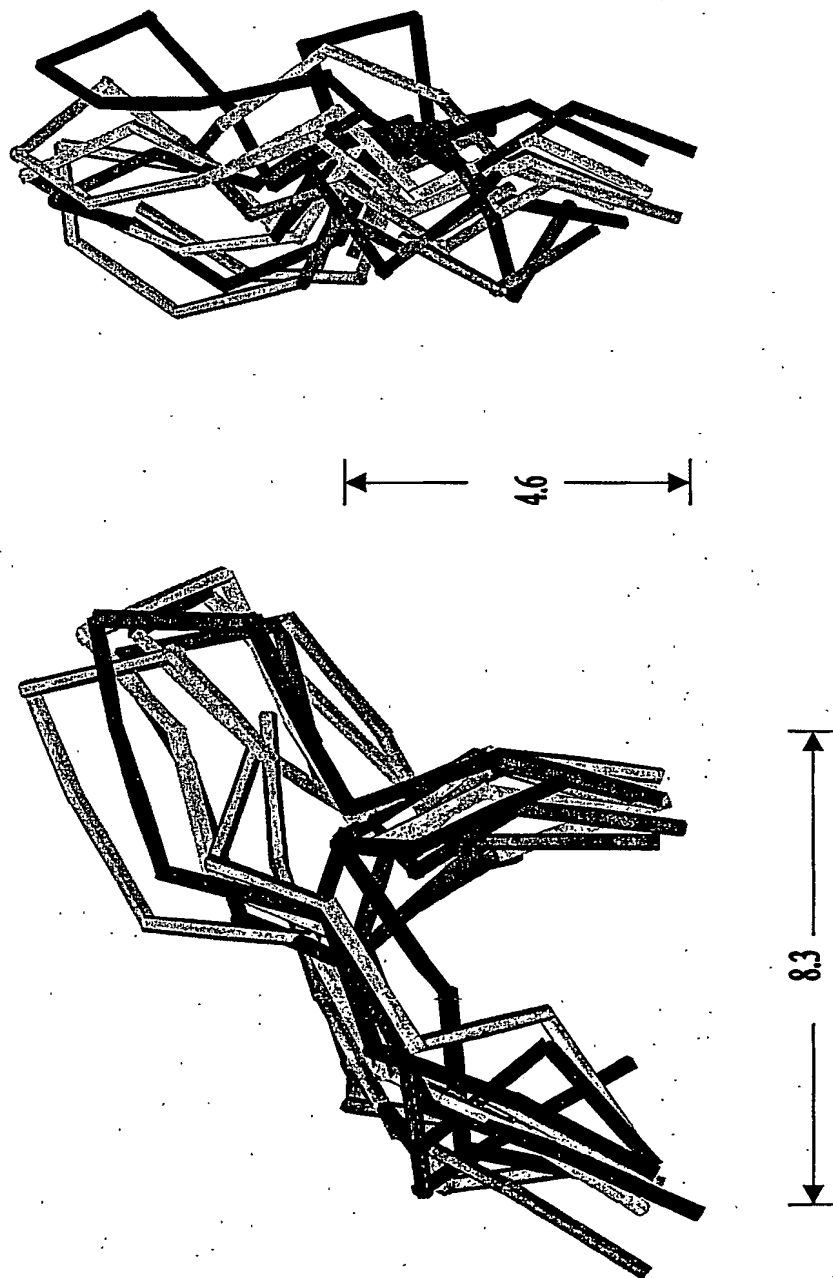


Fig 2g: Residues (292-297) considered as CDLP (C – Domain loop) in different orientations. Dimensions are expressed in Angstrom units.



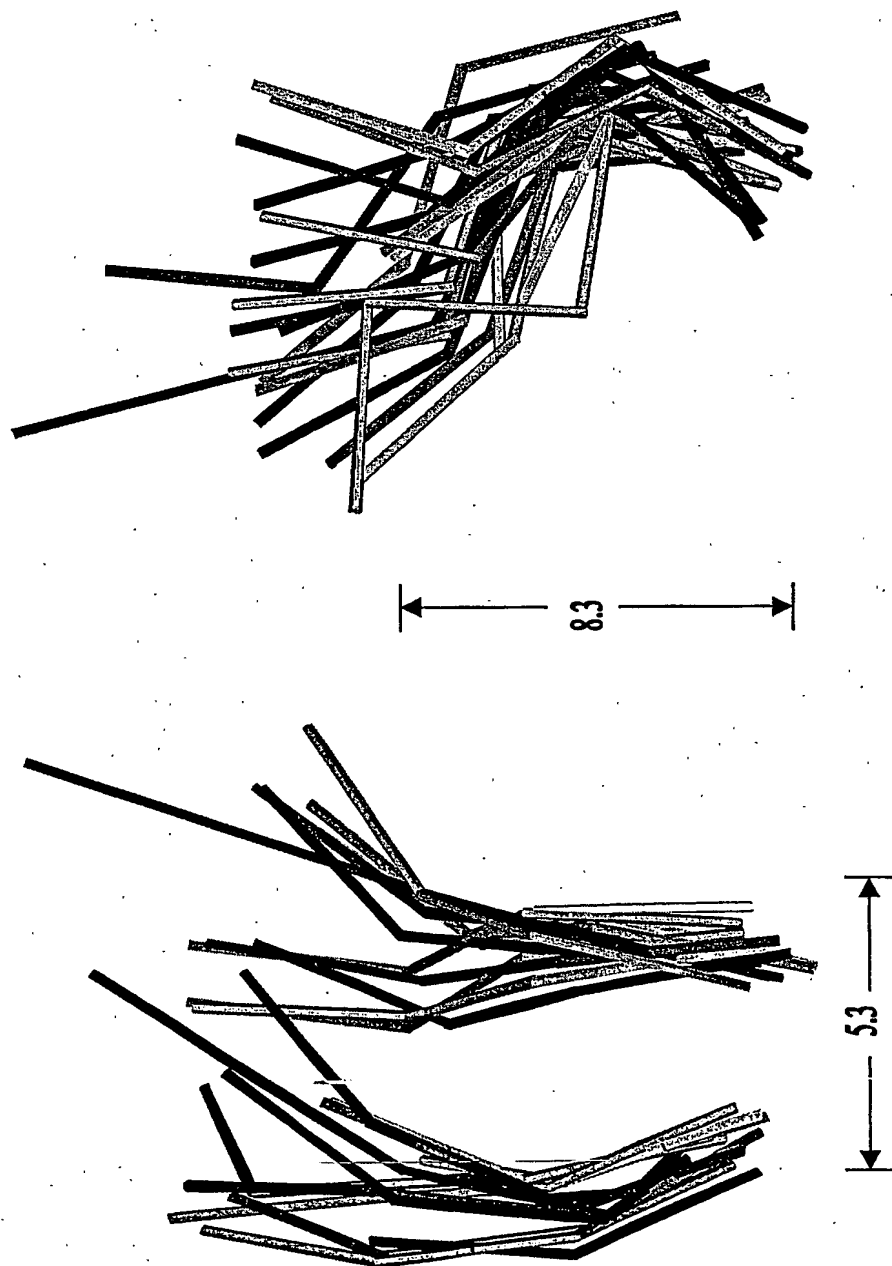


Fig 2h: Residues (277-281, 284-287) considered as SBWL (Substrate Blocking Wall) in different orientations. Dimensions are expressed in Angstrom units.

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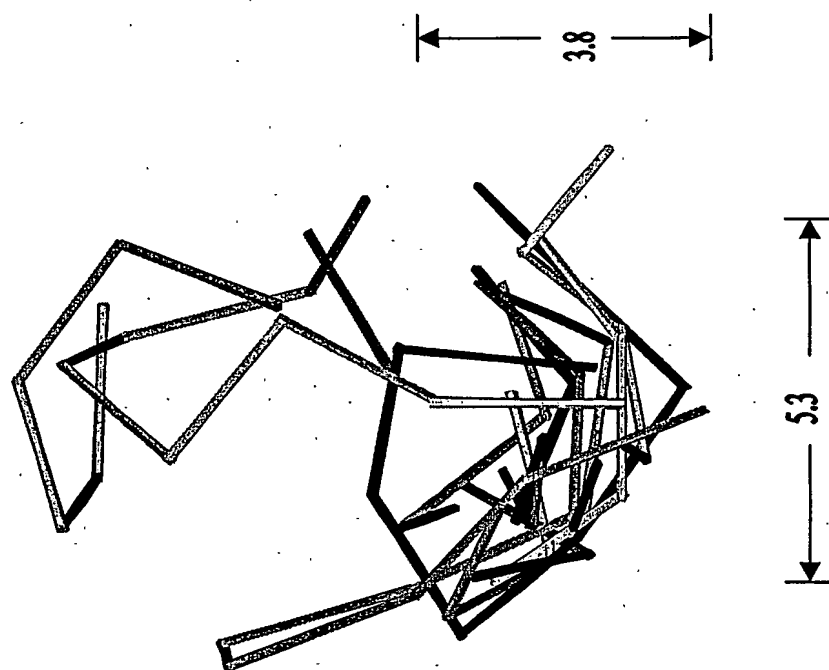


Fig 2i: Residues (281-284) considered as SBLP (Substrate Blocking Loop) in different orientations. Dimensions are expressed in Angstrom units.

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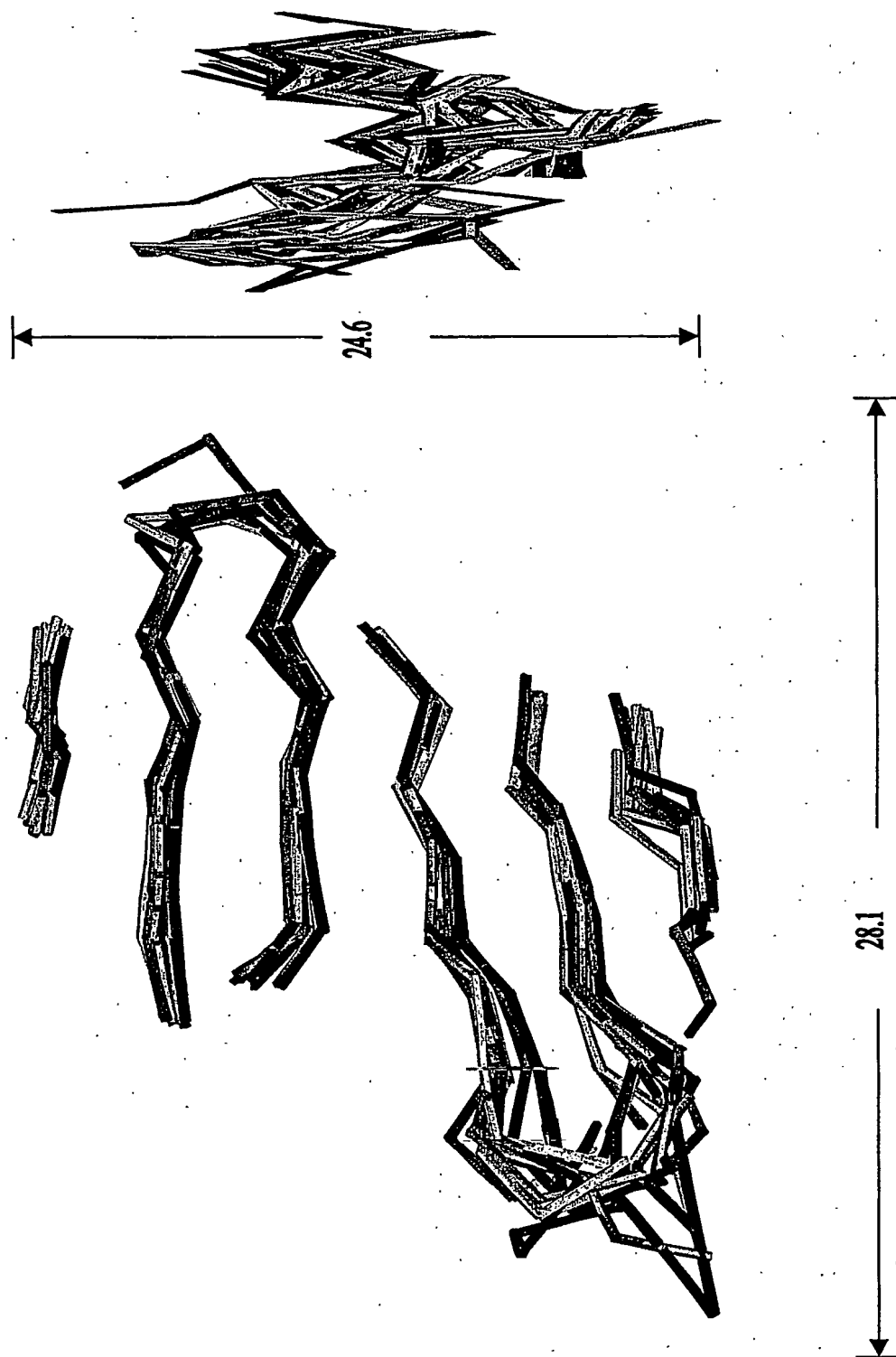
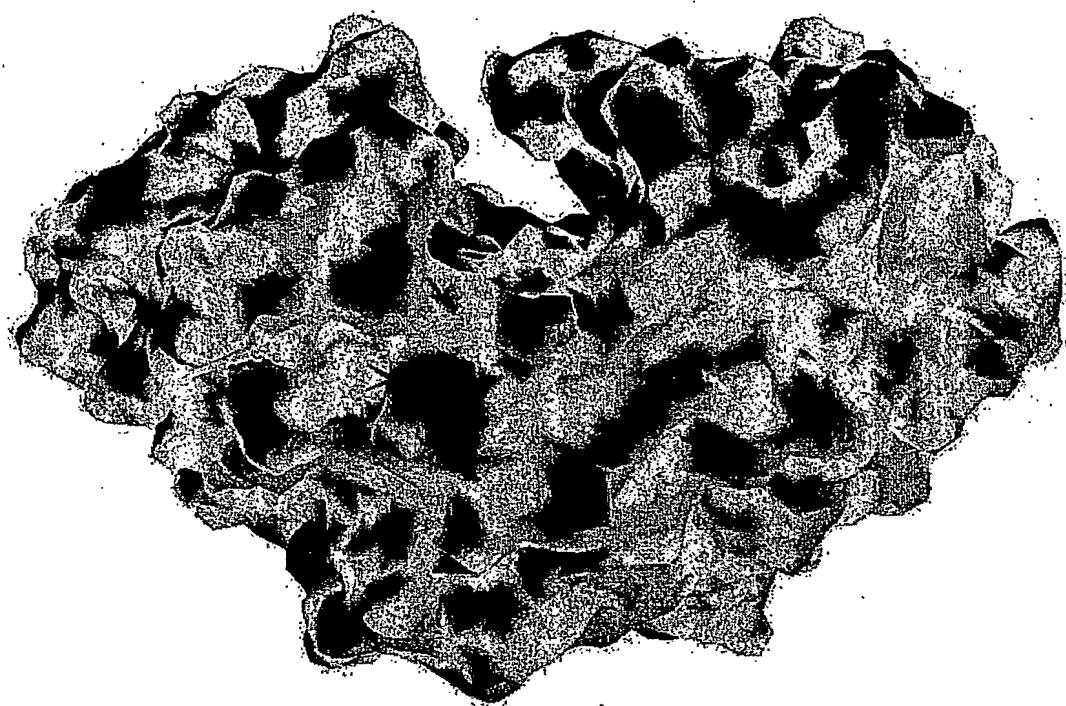
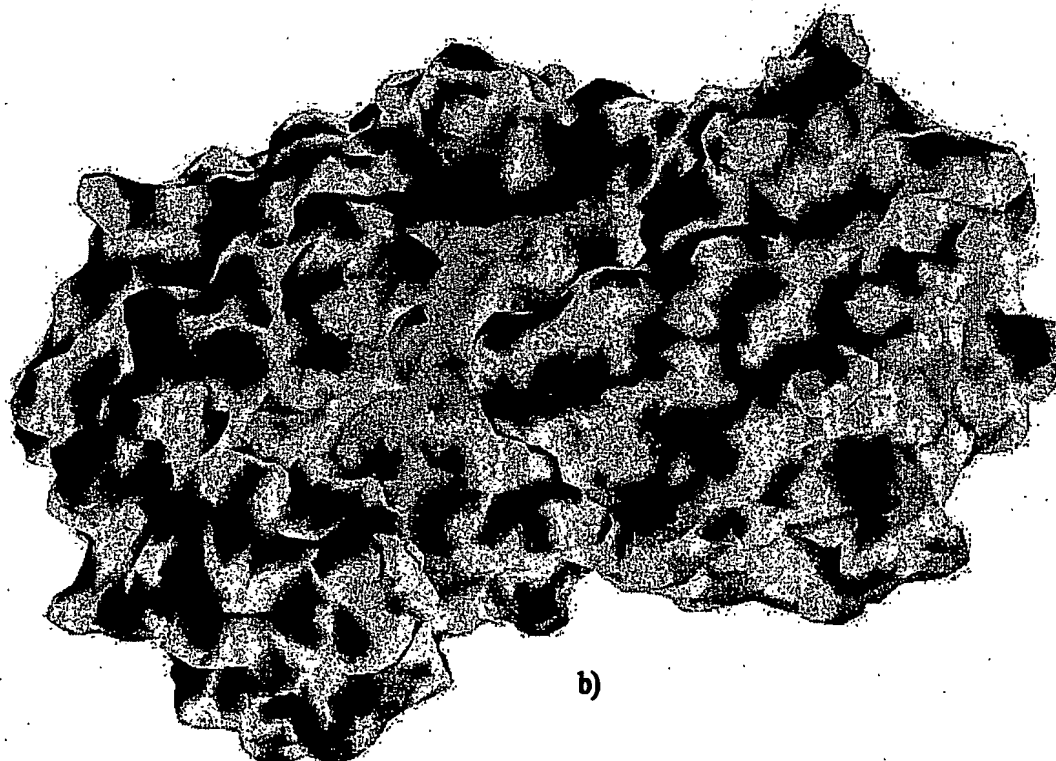


Fig 2j: Residues (5-7, 153-171, 184-187, 307-322) considered as BASE (6-stranded inter domain motif) in different orientations. Dimensions are expressed in Angstrom units.



a)



b)

Fig 3: Surface representation of aspartic proteinase in a) Front view and b) Top view.

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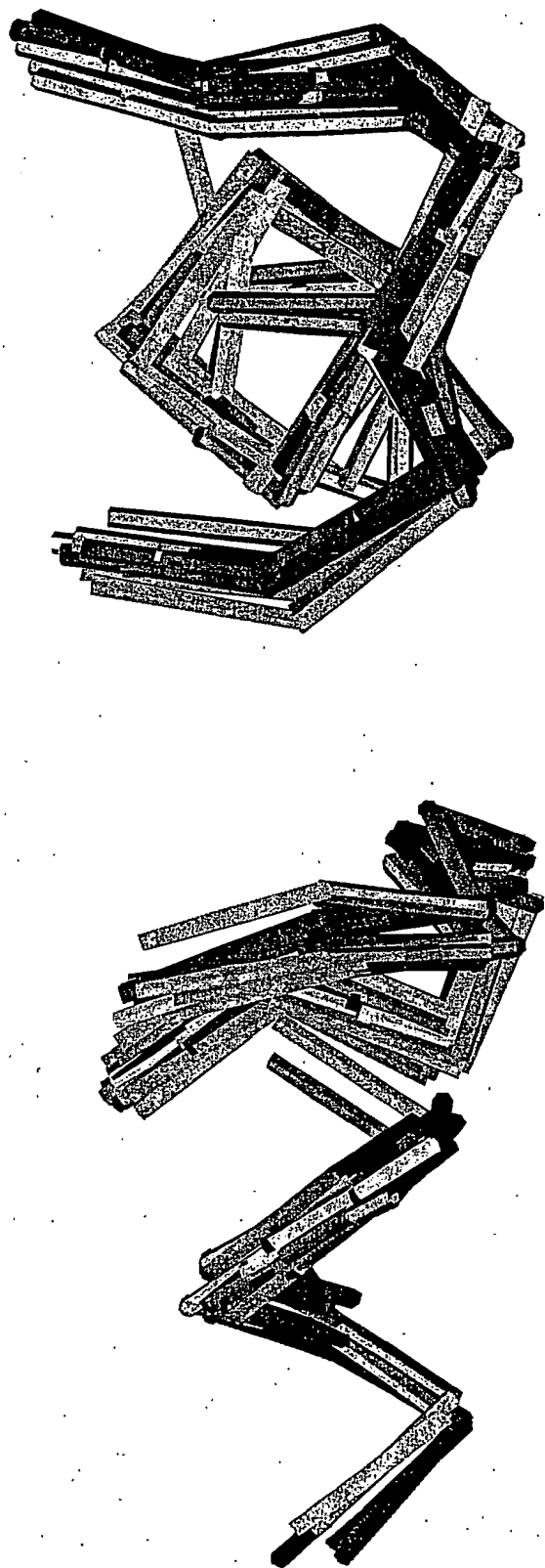


Fig 4a: Two orientations showing the coordination between CDPL and CHEL, probably acting like a 'shock absorber'.

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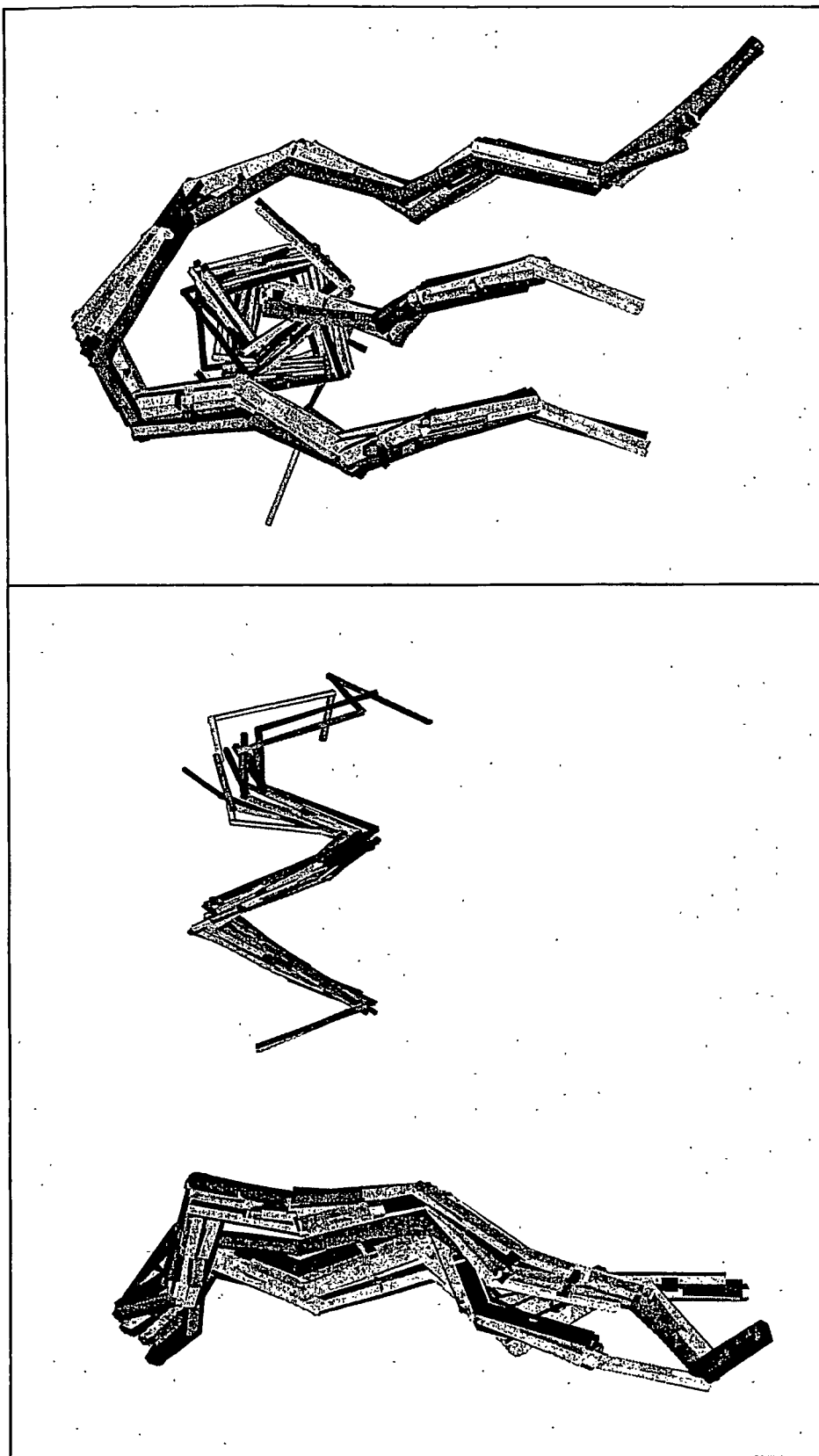
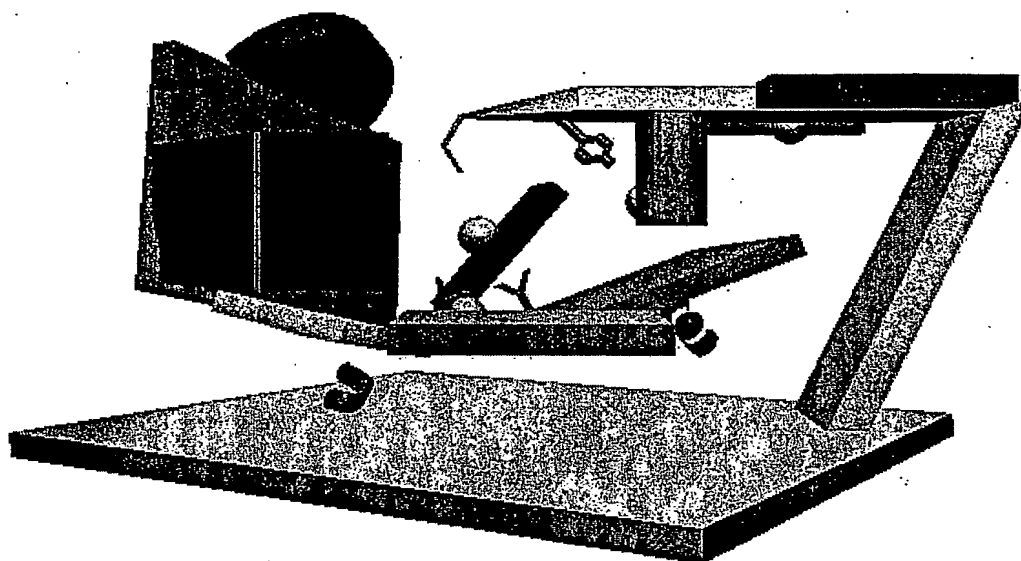
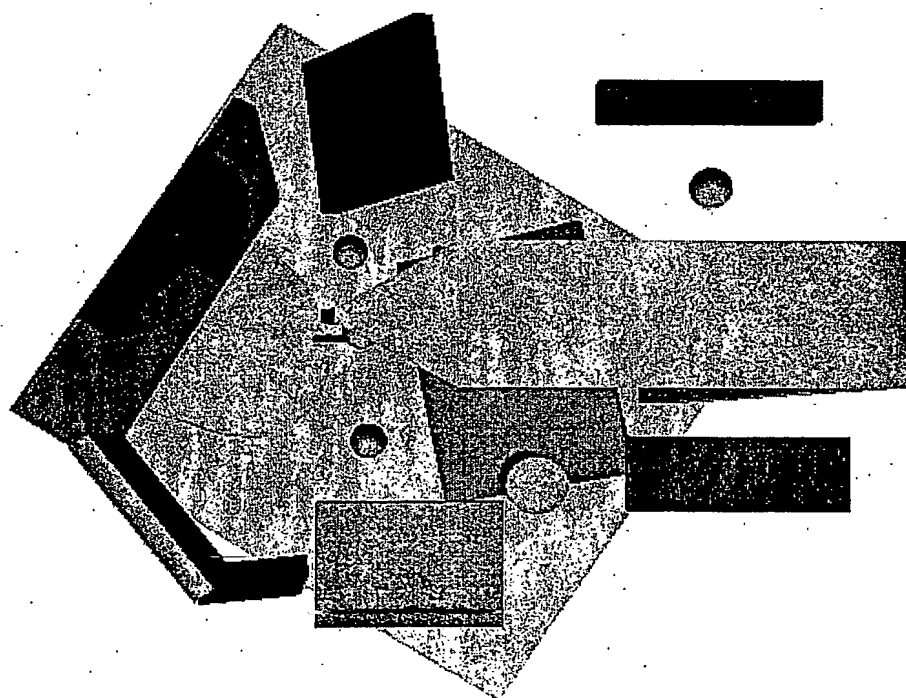


Fig 4b: Two orientations showing the coordination between NDPL and NHLE, probably acting like a 'shock absorber'.

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a)



b)

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Fig 5: PACS representation of aspartic proteinase in a) Front view and b) Top view.

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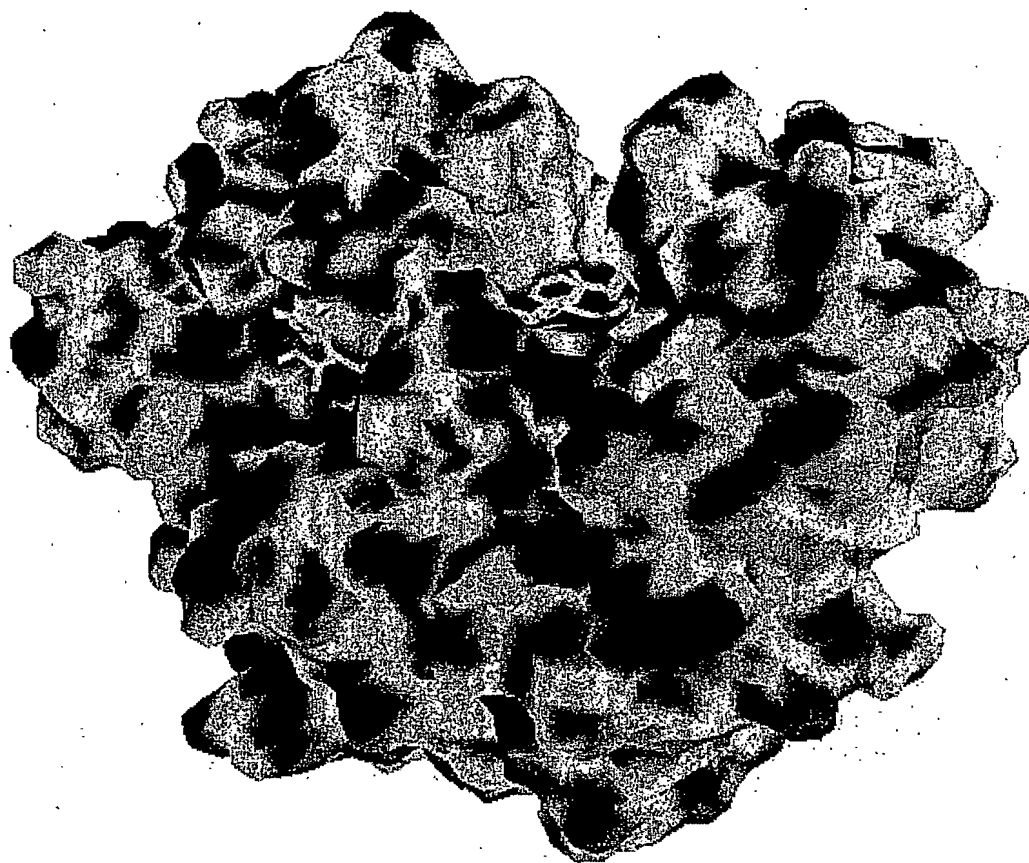


Fig 6: The terminal residues of inhibitor H-261 complexed with endotheiapepsin, projecting out from the exit groove indicating the outlet for the cleaved product of substrate.